

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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Fig. 1

atg gaa tgg atg aga tct aga gtt ggg acc ctg gga .ctg.tgg gtc cga	48
<u>Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly Leu Trp Val Arg</u>	
1 5 10 15	
ctg ctg ctg gct gtc ttc ctg ctg ggg gtc tac caa gca tac ccc atc	96
<u>Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile</u>	
20 25 30	
cct gac tcc agc ccc ctc ctc cag ttt ggg ggt caa gtc cgg cag agg	144
<u>Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg</u>	
35 40 45	
tac ctc tac aca gat gac gac caa gac act gaa gcc cac ctg gag atc	192
<u>Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile</u>	
50 55 60	
agg gag gat gga aca gtg gta ggc gca gca cac cgc agt cca gaa agt	240
<u>Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser</u>	
65 70 75 80	
ctc ctg gag ctc aaa gcc ttg aag cca ggg gtc att caa atc ctg ggt	288
<u>Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly</u>	
85 90 95	
gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat gga gct ctc tat	336
<u>Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr</u>	
100 105 110	
gga tcg cct cac ttt gat cct gag gcc tgc agc ttc aga gaa ctg ctg	384
<u>Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu</u>	
115 120 125	
ctg gag gac ggt tac aat gtg tac cag tct gaa gcc cat ggc ctg ccc	432
<u>Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro</u>	
130 135 140	
ctg cgt ctg cct cag aag gac tcc cca aac cag gat gca aca tcc tgg	480
<u>Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp</u>	
145 150 155 160	
gga cct gtg cgc ttc ctg ccc atg cca ggc ctg ctc cac gag ccc caa	528
<u>Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln</u>	
165 170 175	
gac caa gca gga ttc ctg ccc cca gag ccc cca gat gtg ggc tcc tct	576
<u>Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser</u>	
180 185 190	
gac ccc ctg agc atg gta gag cct tta cag ggc cga agc ccc agc tat	624
<u>Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser Pro Ser Tyr</u>	
195 200 205	
gcg tcc tgactctttc ctgaatcta	649
Ala Ser 1	

662607030405060708090

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Fig. 2A

gaggatccag ccgaaagagg agccaggcac tcaggccacc tgagtctact cacctggaca 60
actggaatct ggcaccaatt ctaaaccact cagcttctcc gagctcacac cccggagatc 120
acctgaggac ccgagccatt g atg gac tcg gac gag acc ggg ttc gag cac 171
Met Asp Ser Asp Glu Thr Gly Phe Glu His
1 5 10
tca gga ctg tgg gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc 219
Ser Gly Leu Trp Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys
15 20 25
cag gca cac ccc atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc 267
Gln Ala His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly
30 35 40
caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa 315
Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu
45 50 55
gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac 363
Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp
60 65 70
cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt 411
Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val
75 80 85 90
att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca 459
Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro
95 100 105
gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc 507
Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser
110 115 120
ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa 555
Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu
125 130 135
gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg 603
Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg
140 145 150
gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg 651
Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu
155 160 165 170
ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc 699
Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro
175 180 185

APPROVED	O.G. FIG.	
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Fig. 2B

gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc 747
Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly
190 195 200

cga agc ccc agc tac gct tcc tga agccagaggc tgtttactat gacatctcct 801
Arg Ser Pro Ser Tyr Ala Ser
205 210

ctttatttat taggttattt atcttattta tttttttatt tttcttactt gagataataa 861
agagttccag aggaggataa gaatgagcat gtgtgagtgt ctgagggaag acatggcagc 921
tgttttgtct cccttgggcc ggacaatccc ctctacacct cccctcacgt ggtccgaggg 981
tcctggcttc ccactgggccc tcactttttt cttttctttt cttttctttt ttttgagacg 1041
gagtctcgct ctgcactcca gccaggcca cagagcgaga ttccatctca aaaaaataaa 1101
taaataaata aataaataaa tataaaaata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1161
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1190

6
5
4
3
2
1
0
1
2
3
4
5
6

APPROVED	O.G. FIG.	
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Fig. 3A

	1					50
hAgg-26257	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~M
mAgg-26257	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~M
Hfgf14	~~~~~	~~~~~	~~MAAAIASG	LIRQKRQARE	QHWDRPSASR	
Mfgf14	~~~~~	~~~~~	~~MAAAIASG	LIRQKRQARE	QHWDRPSASR	
Hfgf12	~~~~~	~~~~~	~~MAAAIASS	LIRQKRQARE	SNSDRVSASK	
Mfgf13	~~~~~	~~~~~	~~MTAAIASS	LIRQKRQARE	R..EKSNAACK	
Hfgf5	~~~~~MS	LSFLLLLLFFS	HLILSAWAHG	EKRLAPKGQP	GPAATDRNPI	
Mfgf5	~~~~~MS	LSLLFLIFCS	HLIHSAWAHG	EKRLTPEGQP	APPRNPGDSS	
Hfgf6	MALGQQLFIT	MSRGAGRLQG	TLWALVFLGI	LVGMVVPSPA	GTRA..NNTL	
Mfgf6	MALGQQLFIT	MSRGAGRVQG	TLQALVFLGV	LVGMVVPSPA	GARA..NGTL	
Hfgf4	~~~~~	~MSGPGTAAV	ALLPAVLLAL	LAPWAGRGGA	AAPTAPNGTL	
Mfgf4	~~~~~	~MAKRGPTTG	TLLPRVLLAL	VVALADRGTG	...APNGTR	
Hfgf3	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mfgf3	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hfgf7	~~~~~	~~~~~	~~~~~	~~~~~	MHKWILTWIL	PTLLYRSCFH
Mfgf7	~~~~~	~~~~~	~~~~~	~~~~~	MRKWILTRIL	PTLLYRSCFH
Hfgf9	~~~~~	~~~~~	~~~~~	~~~~~	MAPLGEVGNV	FGVQDAVPFG
Mfgf9	~~~~~	~~~~~	~~~~~	~~~~~	MAPLGEVGSY	FGVQDAVPFG
Hfgf1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mfgf1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hfgf2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mfgf2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
cons	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	

	51					100
hAgg-26257	DSDETGFEHS	GLWVS.VLAG	LLLGACQAH	IPDSSPLLQF	GGQVRQRYLY	
mAgg-26257	EWMRSRVGTL	GLWVRLLLAV	FLLGVYQAYP	IPDSSPLLQF	GGQVRQRYLY	
Hfgf14	RRSSPSKN.R	GLCNGNLVDI	FSKVRIFGLK	KRRLRRQ.DP	QLKGIVTRLY	
Mfgf14	RRSSPSKN.R	GLFNGNLVDI	FSKVRIFGLK	KRRLRRQ.DP	QLKGIVTRLY	
Hfgf12	RRSSPSKDGR	SLCERHVLGV	FSKVRFCSGR	KRPVRRRPEP	QLKGIVTRLF	
Mfgf13	CVSSPSK.GK	TSCDKNKLNV	FSRVKLFSGK	KRR.RRRPEP	QLKGIVTKLY	
Hfgf5	GSSSRQSSSS	AMSSSSASSS	PAASLGSQGS	GLQSSSFQWS	PSGRRTGSLY	
Mfgf5	GSRGR..SSA	TFSSSSASSP	VAASPGSQGS	GSEHSSFQWS	PSGRRTGSLY	
Hfgf6	LD..SRGWT	LLSRSRAGL.	.AGEI..AGV	NWESG...YL	VGIKRQRRLY	
Mfgf6	LD..SRGWT	LLSRSRAGL.	.AGEI..SGV	NWESG...YL	VGIKRQRRLY	
Hfgf4	EAELERRWES	LVALSLARLP	VAAQP..KEA	AVQSGAGDYL	LGIKRLRRLY	
Mfgf4	HAELGHGWDG	LVARSLARLP	VAAQP..PQA	AVRSGAGDYL	LGLKRLRRLY	
Hfgf3	~MGLIWLLLL	SLLEPGWPA	GPGARLRDA	GGRGGVYEH	GGAPRRRKL	
Mfgf3	~MGLIWLLLL	SLLEPSWPT	GPGLRLRDA	GGRGGVYEH	GGAPRRRKL	
Hfgf7	IICLVGTISL	ACNDMSPEQM	ATNVNCSSPE	RHTRSVDYME	GGDIRVRRLF	
Mfgf7	LVCLVGTISL	ACNDMSPEQT	ATSVNCSSPE	RHTRSVDYME	GGDIRVRRLF	
Hfgf9	NVPVLPVDSP	VLLSDHLGQS	EAGGLPRGPA	.VTDLDHLK.	.GILRRRQLY	
Mfgf9	NVPVLPVDSP	VLLNDHLGQS	EAGGLPRGPA	.VTDLDHLK.	.GILRRRQLY	
Hfgf1	~~~~~	~~~~~MAEG	EITTF TALTE	...KFNLPP	GNYYKKPKLLY	
Mfgf1	~~~~~	~~~~~MAEG	EITTF AALTE	...RFNLPP	GNYYKKPKLLY	
Hfgf2	~~~~~	~~~~~MAAG	SITTL PALPE	.DGGSGAFP	GHFKDPKRLY	
Mfgf2	~~~~~	~~~~~MAAS	GITSL PALPE	.DGGGA.FPP	GHFKDPKRLY	
cons	.sl....sl	.l..s.a.a.	fagv...gp.	..rssl..	ggikrvrrLy	

APPROVED	O.G. FIG.	
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Fig. 3B

	101		150
hAgp-26257	TDDAQQTEAH	LEIREDGTVG	GAADQ.SPES LLQLKALKPG VIQILGVKTS
mAgp-26257	TDDDQDTEAH	LEIREDGTVV	GAAHR.SPES LLELKALKPG VIQILGVKAS
Hfgf14	CR..QGY..Y	LQMHPDGALD	GTKDDSTNST LFNLI PVGLR VVAIQGVKTG
Mfgf14	CR..QGY..Y	LQMHPDGALD	GTKDDSTNST LFNLI PVGLR VVAIQGVKTG
Hfgf12	SQ..QGY..F	LQMHPDGTID	GTKDENS DYT LFNLI PVGLR VVAIQGVKAS
Mfgf13	SR..QGY..H	LQLQADGTID	GTKDEDSTYT LFNLI PVGLR VVAIQGVQTK
Hfgf5	CRVGIGF..H	LQIYPDGKVN	GSHE.ANMLS VLEIFAVSQG IVGIRGVFSN
Mfgf5	CRVGIGF..H	LQIYPDGKVN	GSHE.ASVLS ILEIFAVSQG IVGIRGVFSN
Hfgf6	CNVGIGF..H	LQVLPDGRIS	GTHE.ENPYS LLEISTVERG VVSLFGVRS A
Mfgf6	CNVGIGF..H	LQVPPDGRIS	GTHE.ENPYS LLEISTVERG VVSLFGVKSA
Hfgf4	CNVGIGF..H	LQALPDGRIG	GAHA.DTRDS LLELSPVERG VVSIFGVASR
Mfgf4	CNVGIGF..H	LQVLPDGRIG	GVHA.DTRDS LLELSPVQRG VVSIFGVASR
Hfgf3	CATK..Y..H	LQLHPSGRVN	GSLE.NSAYS ILEITAVEVG IVAIRGLFSG
Mfgf3	CATK..Y..H	LQLHPSGRVN	GSLE.NSAYS ILEITAVEVG IVAIRGLFSG
Hfgf7	CRTQ..W..Y	LRIDKRGKVK	GTQEMKN NYN IMEIRTVAVG IVAIKGVESE
Mfgf7	CRTQ..W..Y	LRIDKRGKVK	GTQEMKN SYN IMEIRTVAVG IVAIKGVESE
Hfgf9	CRT..GF..H	LEIFPNGTIQ	GTRKDHSRFG ILEFISIAVG LVSIRGVDSG
Mfgf9	CRT..GF..H	LEIFPNGTIQ	GTRKDHSRFG ILEFISIAVG LVSIRGVDSG
Hfgf1	CSNG.GH..F	LRILPDGTV D	GTRDRSDQHI QLQLSAESVG EVYIKSTETG
Mfgf1	CSNG.GH..F	LRILPDGTV D	GTRDRSDQHI QLQLSAESAG EVYIKGTETG
Hfgf2	CKNG.GF..F	LRIHDPGRVD	GVREKSDPHI KLQLQAEERG VVSIKGVCAN
Mfgf2	CKNG.GF..F	LRIHDPGRVD	GVREKSDPHV KLQLQAEERG VVSIKGVCAN
cons	cr.g.gf..h	LqihpdG.vd	Gt.e.sspys llel.avevg vv.ikgvksg

	151		200
hAgp-26257	RFLCQRPDGA	LYGSLHFDPE	ACSFRELLLE DGYNVYQSEA HGLPLHLPGN
mAgp-26257	RFLCQQPDGA	LYGSPHFDPE	ACSFRELLLE DGYNVYQSEA HGLPLRLPQK
Hfgf14	LYIAMN GEGY	LYPSELFTPE	.CKFKESVFE NYVVIYSSML YRQQESGRA.
Mfgf14	LYIAMN GEGY	LYPSELFTPE	.CKFKESVFE NYVVIYSSML YRQQESGRA.
Hfgf12	LYVAMN GEGY	LYSSDVFTPE	.CKFKESVFE NYVVIYSSTL YRQQESGRA.
Mfgf13	LYLAMN GEGY	LYTSEHFTPE	.CKFKESVFE NYVVTYSSMI YRQQESGRG.
Hfgf5	KFLAMSKKGK	LHASAKFTDD	.CKFRERFQE NSYNTYASAI HRTEKTGRE.
Mfgf5	KFLAMSKKGK	LHASAKFTDD	.CKFRERFQE NSYNTYASAI HRTEKTGRE.
Hfgf6	LFVAMNSKGR	LYATPSFQEE	.CKFRETL LP NNYNAYESDL Y.....QG.
Mfgf6	LFVAMNSKGR	LYTTPSFHDE	.CKFRETL LP NNYNAYESDL Y.....RG.
Hfgf4	FFVAMSSKGK	LYGSPFFTDE	.CTFKEILLP NNYNAYESYK Y.....PG.
Mfgf4	FFVAMSSRGK	LFGVPFFTDE	.CKFKEILLP NNYNAYEAYA Y.....PG.
Hfgf3	RYLAMNKRGR	LYASEHYSAE	.CEFVERIHE LGYNTYASRL YRTVSSTPGA
Mfgf3	RYLAMNKRGR	LYASDHYN AE	.CEFVERIHE LGYNTYASRL YRTGSSGPGA
Hfgf7	FYLAMNKEGK	LYAKKECNE D	.CNFKELILE NHYNTYASAK WTH..NG...
Mfgf7	FYLAMNKEGK	LYAKKECNE D	.CNFKELILE NHYNTYASAK WTH..SG...
Hfgf9	LYLGMNEKGE	LYGSEKLTQE	.CVFREQFEE NWYNTYSSNL YKHVDTG...
Mfgf9	LYLGMNEKGE	LYGSEKLTQE	.CVFREQFEE NWYNTYSSNL YKHVDTG...
Hfgf1	QYLAMDTDGL	LYGSQTPNEE	.CLFLERLEE NHYNTYISKK H....AE...
Mfgf1	QYLAMDT EGL	LYGSQTPNEE	.CLFLERLEE NHYNTYTSKK H....AE...
Hfgf2	RYLAMKEDGR	LLASKCVTDE	.CFFFERLES NNYNTYRSRK Y....T....
Mfgf2	RYLAMKEDGR	LLASKCVTEE	.CFFFERLES NNYNTYRSRK Y....S....
cons	lylamnk.G.	Lyasehft.e	.CkF.Erll e nnYntY.s.l y....sg...

APPROVED	O.G. FIG.	
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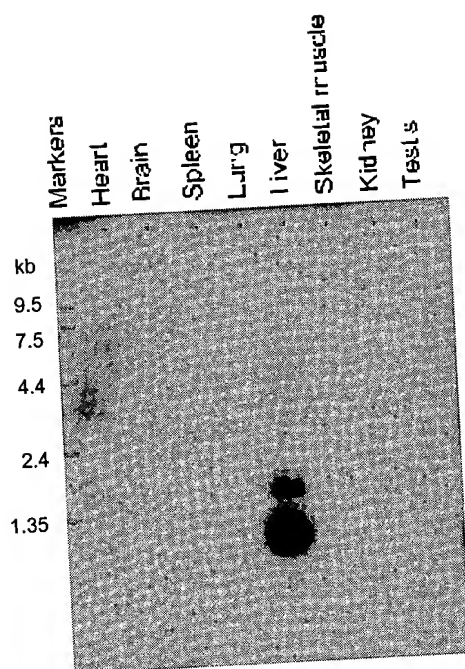
Fig. 3C

	201	250
hAgp-26257	KSPHRDPAPR	GPA...RFLP
mAgp-26257	DSPNQDATSW	GPV...RFLP
Hfgf14W	FLGLNKEGQA
Mfgf14W	FLGLNKEGQV
Hfgf12W	FLGLNKEGQI
Mfgf13W	YLGLNKEGEI
Hfgf5W	YVALNKRKGA
Mfgf5W	YVALNKRKGA
Hfgf6T	YIALSKYGRV
Mfgf6T	YIALSKYGRV
Hfgf4M	FIALSKNGKT
Mfgf4M	FMALSKNGRT
Hfgf3	RRQPSAERLW	YVSVNGKGRP
Mfgf3	QRQPGAQRPW	YVSVNGKGRP
Hfgf7GEM	FVALNQKGIP
Mfgf7GEM	FVALNQKGIP
Hfgf9RRY	YVALNKDGTP
Mfgf9RRY	YVALNKDGTP
Hfgf1KNW	FVGLKKNKSC
Mfgf1KNW	FVGLKKNKSC
Hfgf2SW	YVALKRTGQY
Mfgf2SW	YVALKRTGQY
consw	yvalnk.g.p

	251					300
hAgg-26257	VGPSQGRSPS	YAS~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
mAgg-26257	VEPLQGRSPS	YAS~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hfgf14	SLHDVGETVP	KPGVTPSKST	SASAIMNGGK	PVNKSKTT~	~~~~~	~~~~~
Mfgf14	SLHDVGETVP	KAGVTPSKST	SASAIMNGGK	PVNKCKTT~	~~~~~	~~~~~
Hfgf12	SLHEIGEKGQ	R...SRKS	SGTPTMNGGK	VVNQDST~	~~~~~	~~~~~
Mfgf13	SLHDLTEFSR	SGSGTPTKSR	SVSGVLNGGK	SMSHNEST~	~~~~~	~~~~~
Hfgf5	FTVTVPCKKN	SPSPIKSKIP	LSAPRKNTNS	VKYRLKFRFG	~~~~~	~~~~~
Mfgf5	FTVTVPCKKK	P..PVKPKVP	LSQPRRSPSP	VKYRLKFRFG	~~~~~	~~~~~
Hfgf6	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mfgf6	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hfgf4	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mfgf4	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hfgf3	RQLQSGLPRP	PGKGVQPRRR	RQ.KQSPDNL	EPSHVQASRL	GSQLEASAH~	~~~~~
Mfgf3	RLQSSQPRA	PGEQSQRQR	RQKKQSPGDH	GKMETLSTRA	TPSTQLHTGG	~~~~~
Hfgf7	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mfgf7	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hfgf9	YKDILSQS~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mfgf9	YKDILSQS~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hfgf1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mfgf1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hfgf2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mfgf2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
cons	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~

APPROVED	O.G. FIG.	
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Fig. 4A



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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Fig. 4B

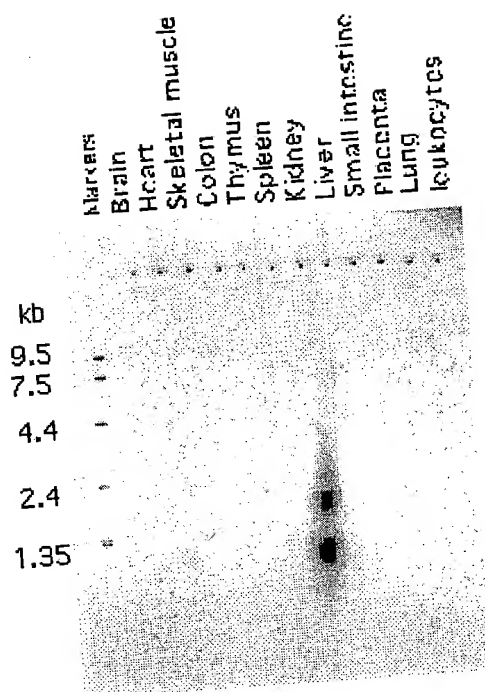
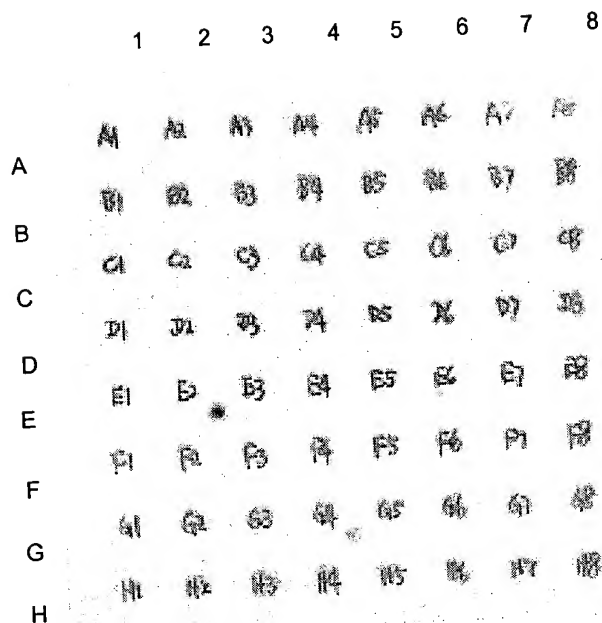


Fig. 4C



	1	2	3	4	5	6	7	8
A	whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippo-campus	medulla oblonggata
B	occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	nucleus accumbens	spinal cord	
C	heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
D	testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
E	kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
F	appendix	lung	trachea	placenta				
G	fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	
H	yeast T-RNA 100 ng	yeast tRNA 100 ng	E. coli rRNA 100 ng	E. coli DNA 100 ng	Poly-(A) 100 ng	human Cot1DNA 100 ng	human DNA 100 ng	human DNA 500 ng